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09/677,042

**IN THE CLAIMS**

Please cancel claims 8 and 10 without prejudice or disclaimer, and amend claim 11 as follows:

1. (Previously Presented) A method for displaying gene expression patterns of multiple genes whose expressions change according to experiment cases, where a first axis represents the genes and a second axis represents gene expression status of the experiment cases, the method comprising the steps of:  
designating a clustering-applied region along the second axis and a segment shorter than a width of the clustering-applied region along the second axis;  
incrementally clustering the expression pattern data by the segment within the clustering-applied region in a forward or reverse direction along the second axis by calculating similarity or dissimilarity for clustering within a clustering range as wide as the segment along the second axis based on a respective reference value set for each clustering range; and  
displaying the results according to a predetermined display format.
2. (Previously Presented) A method for displaying gene expression patterns according to claim 1, further comprising comparing a plurality of expression patterns of every two different genes to determine whether said genes are identical or not.
3. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein some of the multiple genes have the same expression pattern at the beginning of said experiment cases but change to different expression patterns within the clustering-applied region along the second axis.
4. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein some of the multiple genes have different expression patterns at the beginning of said experiment case but change to the same expression pattern within the clustering-applied region along the second axis.
5. (Previously Presented) A method for displaying gene expression patterns according to claim 1, wherein the experiment cases are conducted in a time sequence.